

The motor domain is amino acids 95–348 or base pair 143–1174.

Fig. 1A

601 GGTGTATAATGAACAGATCCATGACCTCCTGGAGCCCAAGGGGCCCCTTGCCATCCGCGA 660  
 -----+-----+-----+-----+-----+-----+-----+  
 uValTyrAsnGluGlnIleHisAspLeuLeuGluProLysGlyProLeuAlaIleArgG1  
 5  
 661 GGACCCCGACAAGGGGGTGGTGGTGAAGGACTTTCTTTCCACCAGCCAGCCTCAGCCGA 720  
 -----+-----+-----+-----+-----+-----+-----+  
 uAspProAspLysGlyValValValGlnGlyLeuSerPheHisGlnProAlaSerAlaG1  
 10  
 721 GCAGCTGCTGGAGATACTGACCAGGGGGAACCGTAACCGCACGCAGCACCCCACTGATGC 780  
 -----+-----+-----+-----+-----+-----+-----+  
 uGlnLeuLeuGluIleLeuThrArgGlyAsnArgAsnArgThrGlnHisProThrAspAl  
 15  
 781 CAACGCGACTTCCTCCCGCTCCCATGCCATCTTCCAGATCTTTGTGAAGCAGCAGGACCG 840  
 -----+-----+-----+-----+-----+-----+-----+  
 aAsnAlaThrSerSerArgSerHisAlaIlePheGlnIlePheValLysGlnGlnAspAr  
 20  
 841 GGTTCAGGACTGACCCAGGCTGTCCAGGTGGCCAAGATGAGCCTGATTGACCTGGCTGG 900  
 -----+-----+-----+-----+-----+-----+-----+  
 gValProGlyLeuThrGlnAlaValGlnValAlaLysMetSerLeuIleAspLeuAlaG1  
 25  
 901 CTCAGAGCGGGCATCCAGCACCCATGCGAAGGGGGAGCGGCTGCGGGAGGGGGCCAACAT 960  
 -----+-----+-----+-----+-----+-----+-----+  
 ySerGluArgAlaSerSerThrHisAlaLysGlyGluArgLeuArgGluGlyAlaAsnIl  
 30  
 961 CAACCGCTCTCTGCTGGCGCTCATCAACGCTCTCAATGCCTTGGCCGATGCAAAGGGCCG 1020  
 -----+-----+-----+-----+-----+-----+-----+  
 eAsnArgSerLeuLeuAlaLeuIleAsnValLeuAsnAlaLeuAlaAspAlaLysGlyAr  
 35  
 1021 CAAGACCCATGTGCCCTACCGGGACAGCAAAGTACCCGCTGCTCAAAGACTCCCTCGG 1080  
 -----+-----+-----+-----+-----+-----+-----+  
 gLysThrHisValProTyrArgAspSerLysLeuThrArgLeuLeuLysAspSerLeuG1  
 40  
 1081 GGGCAACTGCCGCACAGTGATGATCGCTGCCATCAGCCCCTCCAGCCTGACCTACGAGGA 1140  
 -----+-----+-----+-----+-----+-----+-----+  
 yGlyAsnCysArgThrValMetIleAlaAlaIleSerProSerSerLeuThrTyrGluAs  
 45  
 1141 CACGTACAACACCCTCAAATATGCCGACCGGGGCCAAGGAGATCAGGCTCTCGCTGAAGAG 1200  
 -----+-----+-----+-----+-----+-----+-----+  
 pThrTyrAsnThrLeuLysTyrAlaAspArgAlaLysGluIleArgLeuSerLeuLysSe  
 50  
 1201 CAATGTGACCAGCCTGGACTGTACATCAGCCAGTATGCTACCATCTGCCAACAGCTCCA 1260  
 -----+-----+-----+-----+-----+-----+-----+  
 rAsnValThrSerLeuAspCysHisIleSerGlnTyrAlaThrIleCysGlnGlnLeuG1  
 55

Fig. 1B

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1261 GGCTGAGGTAGCCGCTCTGAGGAAGAAGCTCCAAGTGTATGAGGGGGGAGGCCAGCCCCC 1320  
-----+-----+-----+-----+-----+-----+  
nAlaGluValAlaAlaLeuArgLysLysLeuGlnValTyrGluGlyGlyGlyGlnProPr

1321 ACCACAGGACCTCCCAGGATCTCCCAAGTCGGGACCACCACCAGAACACCTTCCCAGCTC 1380  
-----+-----+-----+-----+-----+-----+  
oProGlnAspLeuProGlySerProLysSerGlyProProProGluHisLeuProSerSe

1381 CCCCTTGCCACCCACCCCTCCCAGCCAGCCCTGCACCCAGAGCTCCCTGCAGGGCCTAG 1440  
-----+-----+-----+-----+-----+-----+  
rProLeuProProHisProProSerGlnProCysThrProGluLeuProAlaGlyProAr

1441 AGCCCTTCAAGAGGAGAGTCTGGGGATGGAGGCCAGGTGGAGAGGGCCATGGAAGGGAA 1500  
-----+-----+-----+-----+-----+-----+  
gAlaLeuGlnGluGluSerLeuGlyMetGluAlaGlnValGluArgAlaMetGluGlyAs

1501 CTCTTCAGACCAGGAGCAGTCCCCAGAGGATGAGGATGAAGGCCAGCTGAGGAGGTTC 1560  
-----+-----+-----+-----+-----+-----+  
nSerSerAspGlnGluGlnSerProGluAspGluAspGluGlyProAlaGluGluValPr

1561 AACCCAGATGCCAGAGCAGAACCCACACATGCACTGCCAGAGTCCCCTCGCCTGACCC 1620  
-----+-----+-----+-----+-----+-----+  
oThrGlnMetProGluGlnAsnProThrHisAlaLeuProGluSerProArgLeuThrLe

1621 GCAGCCCAAGCCAGTCGTGGGCCACTTCTCAGCACGGGAAGTGGATGGGGACCGTTCTAA 1680  
-----+-----+-----+-----+-----+-----+  
uGlnProLysProValValGlyHisPheSerAlaArgGluLeuAspGlyAspArgSerLy

1681 GCAGTTGGCCCTAAAGGTGCTGTGCGTTGCCAGCGGCAGTACTCCCTGCTCCAAGCAGC 1740  
-----+-----+-----+-----+-----+-----+  
sGlnLeuAlaLeuLysValLeuCysValAlaGlnArgGlnTyrSerLeuLeuGlnAlaAl

1741 CAACCTCCTGACGCCCCGACATGATCACAGAGTTTGAGACCCTACAGCAGCTGGTGCAAGA 1800  
-----+-----+-----+-----+-----+-----+  
aAsnLeuLeuThrProAspMetIleThrGluPheGluThrLeuGlnGlnLeuValGlnGl

1801 GGAAAAAATTGAGCCTGGGGCAGAGGCCTTGAGGACTTCAGGCCTGGCCAGGGGGGCACC 1860  
-----+-----+-----+-----+-----+-----+  
uGluLysIleGluProGlyAlaGluAlaLeuArgThrSerGlyLeuAlaArgGlyAlaPr

1861 TCTGGCTCAGGAGCTGTGTTTCAGAGTCAATCCCTGTGCCGTCTCCTCTCTGCCAGAGCC 1920  
-----+-----+-----+-----+-----+-----+  
oLeuAlaGlnGluLeuCysSerGluSerIleProValProSerProLeuCysProGluPr

Fig. 1C

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1921 TCCAGGATACACTGGCCCTGTGACCCGACTATGGCGAGGCGACTGAGTGGCCCCCTGCA  
-----+-----+-----+-----+-----+-----+ 1980  
oProGlyTyrThrGlyProValThrArgThrMetAlaArgArgLeuSerGlyProLeuHi

1981 CACCCTGGGAATCCCGCCTGGACCCAACTGCACCCAGCCAGGGGTCCCGATGGCCCAT  
-----+-----+-----+-----+-----+-----+ 2040  
sThrLeuGlyIleProProGlyProAsnCysThrProAlaGlnGlySerArgTrpProMe

2041 GGAGAAGAAGAGGAGGAGACCAAGCGCCTTGGAGGCAGACAGTCCCATGGCCTCAAAGCG  
-----+-----+-----+-----+-----+-----+ 2100  
tGluLysLysArgArgArgProSerAlaLeuGluAlaAspSerProMetAlaSerLysAr

2101 GGGCACCAAGCGCCAGCGCCAGTCCTTCTGCCCTGCCCTAAGGAGAGGGTCTCTGCCTGA  
-----+-----+-----+-----+-----+-----+ 2160  
gGlyThrLysArgGlnArgGlnSerPheLeuProCysLeuArgArgGlySerLeuProAs

2161 CACCCAACCTTCACAGGGGCCAGCACCCCAAGGAGAAAGGGCCTCTCCCCCTGCCA  
-----+-----+-----+-----+-----+-----+ 2220  
pThrGlnProSerGlnGlyProSerThrProLysGlyGluArgAlaSerSerProCysHi

2221 TTCCCCCTCGCGTTTGCCCGCCAGCCAGTCATCAAAAGCCGGGTGCCCTGGGCCCCCTCCGC  
-----+-----+-----+-----+-----+-----+ 2280  
sSerProArgValCysProAlaThrValIleLysSerArgValProLeuGlyProSerAl

2281 CATGCAGAACTGCTCCACCCCGCTGGCTCTGCCCACTCGAGACCTCAATGCCACCTTTGA  
-----+-----+-----+-----+-----+-----+ 2340  
aMetGlnAsnCysSerThrProLeuAlaLeuProThrArgAspLeuAsnAlaThrPheAs

2341 TCTCTCTGAGGAGCCTCCCTCAAAGCCAGTTTCCATGAATGCATTGGCTGGGACAAAAA  
-----+-----+-----+-----+-----+-----+ 2400  
pLeuSerGluGluProProSerLysProSerPheHisGluCysIleGlyTrpAspLysIl

2401 ACCCCAGGAGCTGAGCAGGCTGGACCAGCCCTTCATCCCCAGGGCACCTGTGCCCTGT  
-----+-----+-----+-----+-----+-----+ 2460  
eProGlnGluLeuSerArgLeuAspGlnProPheIleProArgAlaProValProLeuPh

2461 CACCATGAAGGGCCCCAAGCCAACATCTTCCCTCCCTGGGACCTCTGCCTGCAAGAAGAA  
-----+-----+-----+-----+-----+-----+ 2520  
eThrMetLysGlyProLysProThrSerSerLeuProGlyThrSerAlaCysLysLysLy

2521 GCGCGTTGCGAGTTCTCTCAGTCTCCATGGCCGCGAGCCGCATCGCCCGCCTCCCGAGCAG  
-----+-----+-----+-----+-----+-----+ 2580  
sArgValAlaSerSerSerValSerHisGlyArgSerArgIleAlaArgLeuProSerSe

Fig. 1D

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2581 CACTTTGAAGAGGCCAGCTGGGCCCCCTTGTA TCTCCAGAGCTGCCCTTGAGTCCCCTGTG  
-----+-----+-----+-----+-----+ 2640  
rThrLeuLysArgProAlaGlyProLeuValLeuProGluLeuProLeuSerProLeuCy

2641 CCCTAGCAACCGGAGGAATGGAAAGGACCTCATCAGGGTGGGGAGAGCGCTCTCAGCAGG  
-----+-----+-----+-----+-----+ 2700  
sProSerAsnArgArgAsnGlyLysAspLeuIleArgValGlyArgAlaLeuSerAlaGl

2701 GAACGGCGTCACCAAGGTGTCCTGACCGCCAGAATGTCCTGACCACCAAGGTGTCCTAAC  
-----+-----+-----+-----+-----+ 2760  
yAsnGlyValThrLysValSer

2761 CTACCGGCCCCCTCTGCTGGATACCCCTCTTGACCTGTAGCCACCTGCACCAGGAGCTGG  
-----+-----+-----+-----+-----+ 2820

2821 ACCTGCCTTCCTTACCTGGGAGCAATTAGTGCCAACACACCTTTGCTGTATTAACATCCC  
-----+-----+-----+-----+-----+ 2880

2881 TCCCCAGACATCCATCCTGCTACTCACCCCTCTGTTAATCTCCTGTTAACTCAGCTTCTT  
-----+-----+-----+-----+-----+ 2940

2941 GGCATGTACATATTCATTTGTGAGTGTTAATGTGCTGCTGTTTTTTGTTTTTGGTGGTT  
-----+-----+-----+-----+-----+ 3000

3001 TTTGTTTTTTGTTTTTTTGTGTTTGGAGATGGAGTCTTACTCTGTGCGCCAGGCTGGAGTG  
-----+-----+-----+-----+-----+ 3060

3061 CAGTGGTACGATCTTGGCTCACTGCAACCTCCGCCTCCTGGGTCAAGTAATTCTCCTGC  
-----+-----+-----+-----+-----+ 3120

3121 CTCAGCTTTCCAAGTAGCTGGGATTACAGGCACCCATCACCACACCCAGCTAATTTTCGT  
-----+-----+-----+-----+-----+ 3180

3181 CTTTTTAATAGAGAGGGGGTTTTTCCATGTTGGCCAGGCTGGTCTTGAACCTCCTGACCTC  
-----+-----+-----+-----+-----+ 3240

3241 AGGTGATCCGCCTGCCTCAGCTTCCCAAAGTGCTGAGATTACAGGCATGAGCTACCACGC  
-----+-----+-----+-----+-----+ 3300

3301 CTGGCCCGTGTTGCTGTTTTAAAGGTGCTGCCATGTTCCCCCATCTTTTTTTTTTTGAG  
-----+-----+-----+-----+-----+ 3360

Fig. 1E

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3361 ATGGAGTCTCGCTCTGTGCGCCAGGCTGGAGTGCAGTGGTGGCGATCTTGGCTCACTGCA  
-----+-----+-----+-----+-----+-----+ 3420

3421 AGCTCCGCCTCCCAGGTTACACCATTTCTCCTGCCTCAGCCTCCCAAGTAGCTGGGACTA  
-----+-----+-----+-----+-----+-----+ 3480

3481 CAGGCGCCACACCACGCCCCGGCTAATTTTTGTATTTTAGTAGAGATGGGGTTTCAC  
-----+-----+-----+-----+-----+-----+ 3540

3541 CGTGTTAGCCAGGCTGGTCTCGATCTGACCTCATGATCCACCCGCTCGGCCTCCCAAAG  
-----+-----+-----+-----+-----+-----+ 3600

3601 TGCTGGGATTACAGGCGTGAGCCACTGCGCCCGGCCTCCCCTCTCATTTATGATGCCCTC  
-----+-----+-----+-----+-----+-----+ 3660

3661 TGTGCAGGCAGACGGCTCTTGGGCTCTTTCCCCACCTGTCTCTAACACAGGCCCCACGG  
-----+-----+-----+-----+-----+-----+ 3720

3721 TGATGGCCACAGGCAGTAGAGGAGGAATGAGGATGGGTGGGGAGCGGGGAGTCGCGGCT  
-----+-----+-----+-----+-----+-----+ 3780

3781 TGGCTCTTCCTGGTTTCTGAGAGGGACATCTTCATCCCTACTCCCCTTGGTCCCCAACCA  
-----+-----+-----+-----+-----+-----+ 3840

3841 CAGTCCTGGTGAAGATGTGGATGATAATGGTGCCTTGATTTCCAAATGAAGACAGCTTTA  
-----+-----+-----+-----+-----+-----+ 3900

3901 TTGCTTAACTCTATTGTACATAGGATACACGTTCAAGTGTAATAAAGTGTAAGGGGAA  
-----+-----+-----+-----+-----+-----+ 3960

3961 TTCAGGCTTAATGCTGCACCTAGATATAAATGCTAATGATACTTGGGTTTATAGCCTTCT  
-----+-----+-----+-----+-----+-----+ 4020

4021 GATCCTTTATTTCTGCATATATATATAGATATATACATATATTTTGGTATAACAATAAA  
-----+-----+-----+-----+-----+-----+ 4080

4081 CCGTCTCCATCCTTGGGAAAAAAAAAAAA 4108

Fig. 1F.

## DNA sequence of HsKIP3A, motor only

5  
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1	GACAGCACGC	TGCAAGTAGT	GGTACGGGTG	CGGCCCCCCA	CCCCTCGGGA	GCTGGACAGT
61	CAGCGGCGGC	CAGTGGTTCA	GGTGGTGGAC	GAGCGGGTGC	TGGTGTTTAA	CCCTGAGGAG
121	CCCGATGGAG	GGTTCCCTGG	CCTGAAATGG	GGTGGCACCC	ATGATGGCCC	CAAGAAGAAG
181	GGCAAAGACC	TGACGTTTGT	CTTTGACCGG	GTCTTTGGCG	AGGCGGCCAC	CCAACAGGAC
241	GTGTTCCAGC	ACACCACGCA	CAGCGTCCTG	GACAGCTTCC	TCCAGGGCTA	CAACTGCTCA
301	GTGTTTGCCT	ACGGGGCCAC	CGGGGCTGGG	AAGACACACA	CCATGCTGGG	AAGGGAGGGG
361	GACCCCGGCA	TCATGTACCT	GACCACCGTG	GAAGTGTACA	GGCGCCTGGA	GGCCCGCCAG
421	CAGGAGAAGC	ACTTCGAGGT	GCTCATCAGC	TACCAGGAGG	TGTATAATGA	ACAGATCCAT
481	GACCTCCTGG	AGCCCAAGGG	GCCCTTGCC	ATCCGCGAGG	ACCCCGACAA	GGGGGTGGTG
541	GTGCAAGGAC	TTTCTTTCCA	CCAGCCAGCC	TCAGCCGAGC	AGCTGCTGGA	GATACTGACC
601	AGGGGGAACC	GTAACCGCAC	GCAGCACCCC	ACTGATGCCA	ACGCGACTTC	CTCCCGCTCC
661	CATGCCATCT	TCCAGATCTT	TGTGAAGCAG	CAGGACCGGG	TTCCAGGACT	GACCCAGGCT
721	GTCCAGGTGG	CCAAGATGAG	CCTGATTGAC	CTGGCTGGCT	CAGAGCGGGC	ATCCAGCACC
781	CATGCGAAGG	GGGAGCGGCT	GCGGGAGGGG	GCCAACATCA	ACCGCTCTCT	GCTGGCGCTC
841	ATCAACGTCC	TCAATGCCTT	GGCCGATGCA	AAGGGCCGCA	AGACCCATGT	GCCCTACCGG
901	GACAGCAAAC	TGACCCGCCT	GCTCAAAGAC	TCCCTCGGGG	GCAACTGCCG	CACAGTGATG
961	ATCGCTGCCA	TCAGCCCCTC	CAGCCTGACC	TACGAGGACA	CGTACAACAC	CCTC

Fig. 2

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Protein sequence of HsKIP3A, motor only

5           1   DSTLQVVVRV  RPPTPRELDS  QRRPVVQVVD  ERVLVFNPEE  PDGGFPGLKW  GGTHDGPKKK  
          61  GKDLTFVFDR  VFGEAATQQD  VFQHTTHSVL  DSFLQGYNCS  VFAYGATGAG  KTHTMLGREG  
         121  DPGIMYLTTV  ELYRRLEARQ  QEKHFEVLIS  YQEVYNEQIH  DLLEPKGPLA  IREDPDKGVV  
         181  VQGLSFHQPA  SAEQLLEILT  RGNRNRTQHP  TDANATSSRS  HAIFQIFVKQ  QDRVPGLTQA  
         241  VQVAKMSLID  LAGSERASST  HAKGERLREG  ANINRSLLAL  INVLNALADA  KGRKTHVPYR  
         301  DSKLTRLLKD  SLGGNCRTVM  IAAISPSSLT  YEDTYNTL

10   Fig. 3

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Figure 4:

MAVEDSTLQVVVRVRPPTPRELDSQRRPVVQVVDERVLVFNPEEPDGGFPGLKWGGT  
 HDGPKKKGKDLTFVFDRLFGEAATQQDVFOHTTHSVLDSFLQGYNCVVFAYGATGAG  
 KTHTMLGREGDPGIMYLTTVELYRRLEARQQEKHFEVLISYQEVYNEQIHDLLLEPKG  
 5 PLAIREDPDKGVVVQGLSFHQPASAEQLLEILTRGNRNRTQHPTDANATSSRSHAIF  
 QIFVKQQDRVPGLTQAVQVAKMSLIDLAGSERASSTHAKGERLREGANINRSLLALI  
 NVLNALADAKGRKTHVPYRDSKLTRLKDSLGGNCRTVMIAAISPSSTLYEDTYNTL  
 KYADRAKEIRLKGNSKLEGKPIPNPLLGLDSTRTGHHHHHH

- 10 Grayed sequence is derived from the vector (pCRT7/CT, Invitrogen) and contains a V5 epitope and polyhistidine tag.

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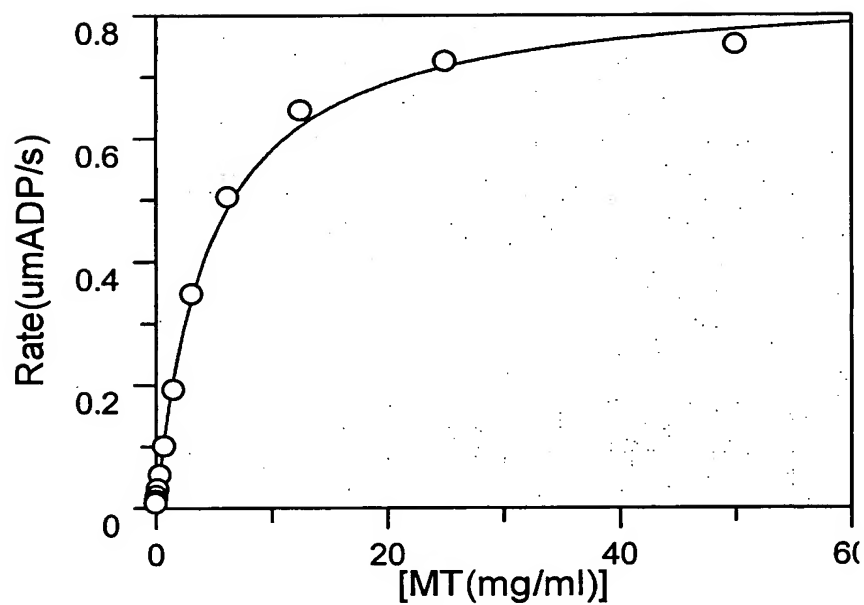
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Figure 5: Nucleotide sequence of the Kip3a fragment used in the ATPase assay

ATGGCAGTGGAGGACAGCACGCTGCAAGTAGTGGTACGGGTGCGGCCCCCACCCT  
CGGGAGCTGGACAGTCAGCGGCGGCCAGTGGTTCAGGTGGTGGACGAGCGGGTGCTG  
5 GTGTTTAACCCTGAGGAGCCCGATGGAGGGTTCCCTGGCCTGAAATGGGGTGGCACC  
CATGATGGCCCCAAGAAGAAGGGCAAAGACCTGACGTTTGTCTTTGACCGGTCTTT  
GGCGAGGCGGCCACCCAACAGGACGTGTTCCAGCACACCACGCACAGCGTCCTGGAC  
AGCTTCCTCCAGGGCTACAACCTGCTCAGTGTTTGCCTACGGGGCCACCGGGGCTGGG  
AAGACACACACCATGCTGGGAAGGGAGGGGGACCCCGGCATCATGTACCTGACCACC  
10 GTGGAACCTGTACAGGCGCCTGGAGGCCCGCCAGCAGGAGAAGCACTTCGAGGTGCTC  
ATCAGCTACCAGGAGGTGTATAATGAACAGATCCATGACCTCCTGGAGCCCAAGGGG  
CCCCTTGCCATCCGCGAGGACCCCGACAAGGGGGTGGTGGTGC AAGGACTTTCCTTTC  
CACCAGCCAGCCTCAGCCGAGCAGCTGCTGGAGATACTGACCAGGGGGAACCGTAAC  
CGCACGCAGCACCCCACTGATGCCAACGCGACTTCCTCCCGCTCCCATGCCATCTTC  
15 CAGATCTTTGTGAAGCAGCAGGACCGGGTTCAGGACTGACCAGGCTGTCCAGGTG  
GCCAAGATGAGCCTGATTGACCTGGCTGGCTCAGAGCGGGCATCCAGCACCCATGCG  
AAGGGGGAGCGGCTGCGGGAGGGGGCCAACATCAACCGCTCTCTGCTGGCGCTCATC  
AACGTCCTCAATGCCTTGCGCGATGCAAAGGGCCGCAAGACCCATGTGCCCTACCGG  
GACAGCAAACCTGACCCGCTGCTCAAAGACTCCCTCGGGGGCAACTGCCGCACAGTG  
20 ATGATCGCTGCCATCAGCCCCTCCAGCCTGACCTACGAGGACACGTACAACACCCTC  
AAATATGCCGACCGGGCCAAGGAGATCAGGCTCAAGGGCAATTCCAAGCTTGAAGGT  
AAGCCTATCCCTAACCCCTCTCCTCGGTCTCGATTCTACGCGTACCGGTCATCATCAC  
CATCACCATTGA

- 25     Grayed sequence is derived from the vector (pCRT7/CT, Invitrogen) and contains a V5 epitope and polyhistidine tag.

Fig. 6



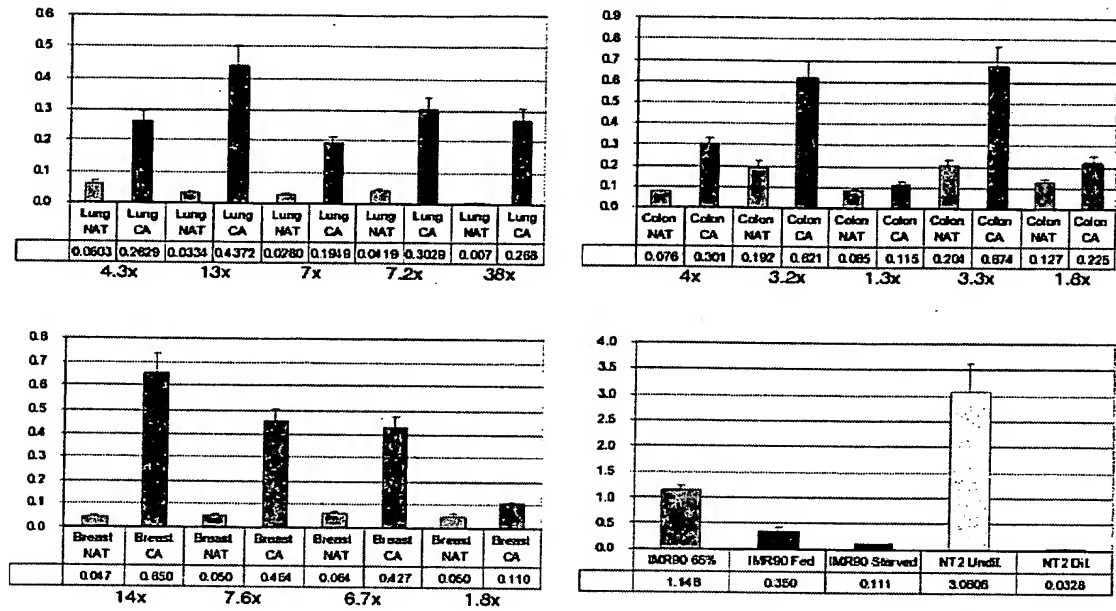
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5 Fig. 7

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